

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	6646588	reduce or reduction or diminish or diminution or decrease or decreased or diminished or reduced	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:44
L2	13851	(factor adj (viii or viiia or eight or "8")) or fviii or fviiia	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:44
L3	2083665	mutant or mutated or modified or variant or analog or allele	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:44
L4	67125	(T adj cell) or T-cell or thymocyte or T-helper	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:44
L5	599063	antigenicity or immunogenicity or reactivity or antigenic or immunogenic or reactive	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:44
L6	4	L1 same L4 same L5 same L2 same L3	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:46
L7	132	(L1 with I5) and (I2 same I3) and I4	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:47
L8	27	((L1 with I5) same I4) and (I2 same I3)	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:47
L9	13851	(factor adj (viii or viiia or eight or "8")) or fviii or fviiia	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:47
L10	211	jacquemin.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:47
L11	11	L10 and L9	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:47

EAST Search History

L12	49340	jones.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:48
L13	13851	(factor adj (viii or viiia or eight or "8")) or fviii or fviiia	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:48
L14	76	L12 and L13	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:48
L15	29	l14 and (l1 same l5)	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:48

SCORE Search Results Details for Application 10511559 and Search Result us-10-511-559-73.rag.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 10:48:54 ; Search time 211 Seconds
(without alignments)
3116.006 Million cell updates/sec

Title: US-10-511-559-73
Perfect score: 7693
Sequence: 1 ATRRYLGAVELSWDYMQSD.....WVHQIALRMEVLGCEAQDLY 1438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
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4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7693	100.0	1438	7	ADM75983	Adm75983 Wild-type
2	7693	100.0	1457	2	AAW46246	Aaw46246 Human fac
3	7693	100.0	1457	2	AAW44372	Aaw44372 Human Fac
4	7693	100.0	1457	8	ADU47569	Adu47569 Human fac
5	7688	99.9	1438	7	ADM75988	Adm75988 Modified
6	7688	99.9	1438	7	ADM75985	Adm75985 Modified
7	7688	99.9	1438	7	ADM75989	Adm75989 Modified
8	7688	99.9	1438	7	ADM75984	Adm75984 Modified
9	7687	99.9	1438	7	ADM75986	Adm75986 Modified
10	7687	99.9	1438	7	ADM75987	Adm75987 Modified
11	7684	99.9	1438	3	AAB01262	Aab01262 B-domain
12	7684	99.9	1438	7	ADF31316	Adf31316 Variant o
13	7684	99.9	1457	2	AAY21675	Aay21675 Beta-doma
14	7684	99.9	1457	7	ADM98124	Adm98124 Human fac
15	7679.5	99.8	1464	8	ADU47624	Adu47624 Human fac
16	7676	99.8	1471	8	ADU47625	Adu47625 Human fac
17	7672	99.7	1479	8	ADU47617	Adu47617 Human fac
18	7668.5	99.7	1440	2	AAR12971	Aar12971 Factor VI
19	7667	99.7	1471	2	AAW23414	Aaw23414 Human B-d
20	7667	99.7	1471	4	AAB67959	Aab67959 Amino aci
21	7666	99.6	1471	8	ADU47608	Adu47608 Human fac
22	7637	99.3	1455	8	ADU47609	Adu47609 Human fac
23	7637	99.3	1461	8	ADU47616	Adu47616 Human fac
24	7635	99.2	1459	4	AAE10832	Aae10832 Human fac
25	7627.5	99.1	1568	8	ADU47621	Adu47621 Human fac
26	7625	99.1	1440	8	ADQ37592	Adq37592 Human Fac
27	7625	99.1	1459	4	AAE10833	Aae10833 Human fac
28	7622	99.1	1459	4	AAE10827	Aae10827 Human fac
29	7620.5	99.1	1516	1	AAP80265	Aap80265 Modified
30	7619	99.0	1585	8	ADU47607	Adu47607 Human fac
31	7619	99.0	1585	8	ADU47613	Adu47613 Human fac
32	7614.5	99.0	1447	8	ADQ37595	Adq37595 Human Fac
33	7614	99.0	1428	8	ADQ37589	Adq37589 Human Fac
34	7614	99.0	1440	8	ADQ37607	Adq37607 Human Fac
35	7610	98.9	1453	8	ADU47619	Adu47619 Human fac
36	7604.5	98.8	1450	8	ADU47615	Adu47615 Human fac
37	7603.5	98.8	1437	8	ADQ37593	Adq37593 Human Fac
38	7603.5	98.8	1447	8	ADQ37610	Adq37610 Human Fac
39	7603	98.8	1428	8	ADQ37604	Adq37604 Human Fac
40	7603	98.8	1444	8	ADQ37596	Adq37596 Human Fac
41	7603	98.8	1457	8	ADU47622	Adu47622 Human fac
42	7601	98.8	1424	4	AAB48842	Aab48842 Mutant ma
43	7601	98.8	1424	5	AAO18622	Aao18622 Human mat
44	7601	98.8	1424	9	ADZ65051	Adz65051 Human mat
45	7599.5	98.8	1441	8	ADQ37597	Adq37597 Human Fac

ALIGNMENTS

RESULT 1

ADM75983

ID ADM75983 standard; protein; 1438 AA.

XX

AC ADM75983;

XX

DT 03-JUN-2004 (first entry)

SCORE Search Results Details for Application 10511559 and Search Result us-10-511-559-73.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 10:59:22 ; Search time 56 Seconds
(without alignments)
2247.661 Million cell updates/sec

Title: US-10-511-559-73
Perfect score: 7693
Sequence: 1 ATTRYYLGAVELSWDYMQSD.....WVHQIALRMEVLGCEAQDLY 1438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
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6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	7693	100.0	1457	2 US-09-001-039B-47	Sequence 47, Appl

2	7684	99.9	1438	2	US-09-209-916-1	Sequence 1, Appli
3	7667	99.7	1471	1	US-08-683-839B-3	Sequence 3, Appli
4	7597	98.8	1447	2	US-09-407-605-4	Sequence 4, Appli
5	7587	98.6	1445	2	US-09-407-605-3	Sequence 3, Appli
6	7443	96.8	1661	1	US-08-882-083-2	Sequence 2, Appli
7	7443	96.8	1661	1	US-08-558-107-2	Sequence 2, Appli
8	7443	96.8	1661	2	US-09-243-539-2	Sequence 2, Appli
9	7236	94.1	2332	2	US-10-360-101-229	Sequence 229, App
10	7236	94.1	2351	1	US-08-366-851A-2	Sequence 2, Appli
11	7236	94.1	2351	2	US-10-133-907-4	Sequence 4, Appli
12	7236	94.1	2351	2	US-09-001-039B-45	Sequence 45, Appl
13	7233	94.0	2332	1	US-08-276-594A-2	Sequence 2, Appli
14	7230	94.0	2351	7	5171844-2	Patent No. 5171844
15	7227	93.9	2332	1	US-07-864-004B-4	Sequence 4, Appli
16	7227	93.9	2332	1	US-08-251-937A-4	Sequence 4, Appli
17	7227	93.9	2332	1	US-08-212-133A-2	Sequence 2, Appli
18	7227	93.9	2332	1	US-08-474-503-2	Sequence 2, Appli
19	7227	93.9	2332	1	US-08-670-707A-2	Sequence 2, Appli
20	7227	93.9	2332	2	US-09-037-601-2	Sequence 2, Appli
21	7227	93.9	2332	2	US-09-315-179-2	Sequence 2, Appli
22	7227	93.9	2332	2	US-09-523-656-2	Sequence 2, Appli
23	7227	93.9	2332	2	US-09-957-641A-2	Sequence 2, Appli
24	7227	93.9	2332	3	US-10-187-319-2	Sequence 2, Appli
25	7227	93.9	2332	3	US-10-131-510A-2	Sequence 2, Appli
26	7227	93.9	2332	5	PCT-US93-03275-4	Sequence 4, Appli
27	7227	93.9	2332	5	PCT-US94-13200-2	Sequence 2, Appli
28	7227	93.9	2351	1	US-08-121-202-2	Sequence 2, Appli
29	7218	93.8	2351	7	5422260-1	Patent No. 5422260
30	7188	93.4	2332	2	US-09-324-867-3	Sequence 3, Appli
31	6569	85.4	1467	2	US-09-523-656-38	Sequence 38, Appl
32	6498	84.5	1443	1	US-08-670-707A-39	Sequence 39, Appl
33	6498	84.5	1443	2	US-09-037-601-39	Sequence 39, Appl
34	6498	84.5	1443	2	US-09-315-179-39	Sequence 39, Appl
35	6498	84.5	1443	3	US-10-187-319-39	Sequence 39, Appl
36	6498	84.5	1443	3	US-10-131-510A-39	Sequence 39, Appl
37	6281	81.6	2343	2	US-09-324-867-2	Sequence 2, Appli
38	6236	81.1	2133	1	US-08-670-707A-37	Sequence 37, Appl
39	6236	81.1	2133	2	US-09-037-601-37	Sequence 37, Appl
40	6236	81.1	2133	2	US-09-315-179-37	Sequence 37, Appl
41	6236	81.1	2133	2	US-09-523-656-30	Sequence 30, Appl
42	6236	81.1	2133	3	US-10-187-319-37	Sequence 37, Appl
43	6236	81.1	2133	3	US-10-131-510A-37	Sequence 37, Appl
44	6201	80.6	2319	1	US-08-212-133A-8	Sequence 8, Appli
45	6201	80.6	2319	1	US-08-474-503-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-001-039B-47

; Sequence 47, Application US/09001039B

; Patent No. 6818439

; GENERAL INFORMATION:

; APPLICANT: Jolly, Douglas J.

; APPLICANT: Chang, Stephen M.W.

; APPLICANT: Respass, James G.

; APPLICANT: DePolo, Nicholas J.

; APPLICANT: Hsu, David Chi-Tang

; APPLICANT: Ibanez, Carlos E.

; APPLICANT: Greengard, Judith

SCORE Search Results Details for Application 10511559 and Search Result us-10-511-559-73.rapbm.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:11:10 ; Search time 205 Seconds
(without alignments)
3249.283 Million cell updates/sec

Title: US-10-511-559-73
Perfect score: 7693
Sequence: 1 ATRRYLGAVELSWDYMQSD.....WVHQIALRMEVLGCEAQDLY 1438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID	Description	

1	7693	100.0	1438	5	US-10-511-559-73	Sequence 73, Appl
2	7684	99.9	1438	4	US-10-006-091-1	Sequence 1, Appli
3	7684	99.9	1438	4	US-10-047-257-1	Sequence 1, Appli
4	7684	99.9	1438	4	US-10-225-900-1	Sequence 1, Appli
5	7684	99.9	1457	5	US-10-813-507-13	Sequence 13, Appl
6	7667	99.7	1471	4	US-10-095-718-2	Sequence 2, Appli
7	7667	99.7	1471	4	US-10-681-970-2	Sequence 2, Appli
8	7635	99.2	1459	4	US-10-239-498A-13	Sequence 13, Appl
9	7625	99.1	1459	4	US-10-239-498A-15	Sequence 15, Appl
10	7622	99.1	1459	4	US-10-239-498A-4	Sequence 4, Appli
11	7601	98.8	1424	5	US-10-472-516-5	Sequence 5, Appli
12	7601	98.8	1424	5	US-10-968-286-5	Sequence 5, Appli
13	7282	94.7	1457	5	US-10-813-507-17	Sequence 17, Appl
14	7236	94.1	2332	4	US-10-360-101-229	Sequence 229, App
15	7236	94.1	2332	4	US-10-466-998A-1	Sequence 1, Appli
16	7236	94.1	2332	4	US-10-721-997A-34	Sequence 34, Appl
17	7236	94.1	2332	5	US-10-789-956-2	Sequence 2, Appli
18	7236	94.1	2351	4	US-10-132-829-4	Sequence 4, Appli
19	7236	94.1	2351	4	US-10-172-712-27	Sequence 27, Appl
20	7236	94.1	2351	4	US-10-133-907-4	Sequence 4, Appli
21	7236	94.1	2351	4	US-10-411-037-30	Sequence 30, Appl
22	7236	94.1	2351	4	US-10-411-026-30	Sequence 30, Appl
23	7236	94.1	2351	4	US-10-410-962-30	Sequence 30, Appl
24	7236	94.1	2351	4	US-10-411-049-30	Sequence 30, Appl
25	7236	94.1	2351	4	US-10-410-930-30	Sequence 30, Appl
26	7236	94.1	2351	4	US-10-410-997-30	Sequence 30, Appl
27	7236	94.1	2351	4	US-10-411-012-30	Sequence 30, Appl
28	7236	94.1	2351	4	US-10-287-994-30	Sequence 30, Appl
29	7236	94.1	2351	4	US-10-410-913-30	Sequence 30, Appl
30	7236	94.1	2351	5	US-10-789-956-1	Sequence 1, Appli
31	7236	94.1	2351	5	US-10-472-516-2	Sequence 2, Appli
32	7236	94.1	2351	5	US-10-410-980-30	Sequence 30, Appl
33	7236	94.1	2351	5	US-10-410-897-30	Sequence 30, Appl
34	7236	94.1	2351	5	US-10-968-286-2	Sequence 2, Appli
35	7236	94.1	2351	5	US-10-492-261-30	Sequence 30, Appl
36	7236	94.1	2351	6	US-11-183-205-30	Sequence 30, Appl
37	7236	94.1	2351	6	US-11-244-087-3	Sequence 3, Appli
38	7236	94.1	2351	6	US-11-267-631-49	Sequence 49, Appl
39	7227	93.9	2332	3	US-09-957-641-2	Sequence 2, Appli
40	7227	93.9	2332	4	US-10-187-319-2	Sequence 2, Appli
41	7227	93.9	2332	4	US-10-131-510A-2	Sequence 2, Appli
42	7227	93.9	2332	4	US-10-445-235-2	Sequence 2, Appli
43	7227	93.9	2332	4	US-10-239-498A-2	Sequence 2, Appli
44	7227	93.9	2332	4	US-10-353-753-1	Sequence 1, Appli
45	7227	93.9	2332	5	US-10-491-464-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-10-511-559-73

; Sequence 73, Application US/10511559

; Publication No. US20050256304A1

; GENERAL INFORMATION:

; APPLICANT: JONES, Tim

; APPLICANT: BAKER, Matthew

; APPLICANT: CARR, Francis, J.

; TITLE OF INVENTION: MODIFIED FACTOR VIII

; FILE REFERENCE: MER-133

; CURRENT APPLICATION NUMBER: US/10/511,559

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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:12:02 ; Search time 16 Seconds
(without alignments)
1000.968 Million cell updates/sec

Title: US-10-511-559-73
Perfect score: 7693
Sequence: 1 ATRRYLGAVELSWDYMQSD.....WVHQIALRMEVLGCEAQDLY 1438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	7693	100.0	1457	7 US-11-280-757-37	Sequence 37, Appl

2	7236	94.1	2351	7	US-11-183-218-30	Sequence 30, Appl
3	7236	94.1	2351	7	US-11-280-757-35	Sequence 35, Appl
4	588	7.6	379	7	US-11-293-697-3405	Sequence 3405, Ap
5	285.5	3.7	524	7	US-11-293-697-3442	Sequence 3442, Ap
6	217	2.8	734	7	US-11-242-505A-24	Sequence 24, Appl
7	212	2.8	734	6	US-10-196-749-458	Sequence 458, App
8	136	1.8	370	7	US-11-293-697-4818	Sequence 4818, Ap
9	122	1.6	364	6	US-10-505-928-605	Sequence 605, App
10	121	1.6	5738	6	US-10-505-928-150	Sequence 150, App
11	119.5	1.6	540	6	US-10-953-349-22757	Sequence 22757, A
12	109	1.4	1575	6	US-10-505-928-257	Sequence 257, App
13	106	1.4	961	6	US-10-548-484-76	Sequence 76, Appl
14	102.5	1.3	735	6	US-10-953-349-5895	Sequence 5895, Ap
15	102.5	1.3	765	6	US-10-953-349-5894	Sequence 5894, Ap
16	102.5	1.3	821	6	US-10-953-349-5893	Sequence 5893, Ap
17	102	1.3	3882	6	US-10-953-349-5549	Sequence 5549, Ap
18	102	1.3	3978	6	US-10-953-349-5548	Sequence 5548, Ap
19	102	1.3	4118	6	US-10-953-349-5547	Sequence 5547, Ap
20	100.5	1.3	690	6	US-10-953-349-1493	Sequence 1493, Ap
21	100.5	1.3	729	6	US-10-953-349-1492	Sequence 1492, Ap
22	100.5	1.3	735	6	US-10-953-349-1491	Sequence 1491, Ap
23	99.5	1.3	541	6	US-10-953-349-8820	Sequence 8820, Ap
24	99.5	1.3	544	6	US-10-953-349-2547	Sequence 2547, Ap
25	99.5	1.3	546	6	US-10-953-349-2546	Sequence 2546, Ap
26	99.5	1.3	592	6	US-10-953-349-3845	Sequence 3845, Ap
27	99.5	1.3	1534	6	US-10-505-928-40	Sequence 40, Appl
28	99	1.3	495	6	US-10-953-349-6931	Sequence 6931, Ap
29	99	1.3	497	6	US-10-953-349-6930	Sequence 6930, Ap
30	99	1.3	507	6	US-10-953-349-6929	Sequence 6929, Ap
31	99	1.3	666	6	US-10-953-349-24660	Sequence 24660, A
32	99	1.3	696	6	US-10-953-349-24659	Sequence 24659, A
33	99	1.3	716	6	US-10-953-349-24658	Sequence 24658, A
34	98	1.3	698	7	US-11-293-697-4312	Sequence 4312, Ap
35	97	1.3	329	6	US-10-953-349-16881	Sequence 16881, A
36	96.5	1.3	591	7	US-11-045-540-1	Sequence 1, Appli
37	96.5	1.3	670	7	US-11-121-154-59	Sequence 59, Appl
38	96.5	1.3	1194	7	US-11-045-540-2	Sequence 2, Appli
39	96.5	1.3	1205	7	US-11-045-540-3	Sequence 3, Appli
40	96.5	1.3	1237	7	US-11-045-540-4	Sequence 4, Appli
41	96.5	1.3	1248	7	US-11-045-540-5	Sequence 5, Appli
42	96	1.2	1344	7	US-11-314-018-20	Sequence 20, Appl
43	96	1.2	1531	6	US-10-505-928-217	Sequence 217, App
44	95.5	1.2	566	6	US-10-548-484-83	Sequence 83, Appl
45	95	1.2	1042	6	US-10-548-484-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1

US-11-280-757-37

; Sequence 37, Application US/11280757

; Publication No. US20060099685A1

; GENERAL INFORMATION:

; APPLICANT: Crucell Holland B.V.

; APPLICANT: Bout, Abraham

; APPLICANT: Opstelten, Dirk-Jan

; APPLICANT: Yallop, Christopher

; TITLE OF INVENTION: RECOMBINANT EXPRESSION OF FACTOR VIII IN HUMAN CELLS

; FILE REFERENCE: 0034 D US P00 CIP

; CURRENT APPLICATION NUMBER: US/11/280,757

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OM protein - protein search, using sw model

Run on: May 25, 2006, 10:52:56 ; Search time 53 Seconds
(without alignments)
2610.560 Million cell updates/sec

Title: US-10-511-559-73
Perfect score: 7693
Sequence: 1 ATRRYYLGAVELSWDYMQSD.....VWHQIALRMEVLGCEAQDLY 1438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	7236	94.1	2351	1	EZHU	coagulation factor	
2	6236	81.1	2133	2	T42763	coagulation factor	
3	6201	80.6	2319	2	A47004	coagulation factor	
4	2391.5	31.1	2224	1	KFHU5	coagulation factor	
5	2371	30.8	2183	2	T42764	coagulation factor	
6	2370	30.8	2211	1	KFBO5	coagulation factor	
7	1740.5	22.6	1069	1	KUHU	ferroxidase (EC 1.	
8	1696.5	22.1	1059	1	A35210	ferroxidase (EC 1.	

9	1104	14.4	216	2	A44258	factor VIII-associ
10	663	8.6	427	2	JC4915	ags protein precur
11	657	8.5	463	1	A36479	milk fat globule m
12	650	8.4	409	2	T11743	pP47 protein - pig
13	635	8.3	401	2	S65138	glycoprotein antig
14	635	8.3	427	2	S74211	PAS-6/7 protein pr
15	543	7.1	869	2	A25945	coagulation factor
16	443	5.8	927	1	JQ0948	A5 antigen precurs
17	424.5	5.5	218	2	A47285	milk fat globule p
18	306.5	4.0	3133	2	S52093	hemocytin - silkwo
19	262	3.4	845	2	JC5256	adipocyte transcri
20	221	2.9	719	2	S51739	transcription repr
21	211	2.7	1283	2	T13799	neurexin IV - frui
22	207.5	2.7	737	2	T31349	hypothetical prote
23	206.5	2.7	737	2	T15615	hypothetical prote
24	193	2.5	913	2	A48280	receptor tyrosine
25	192	2.5	876	2	A49508	protein-tyrosine k
26	185.5	2.4	855	2	S42621	protein-tyrosine k
27	185.5	2.4	910	2	A53137	tyrosine kinase re
28	173.5	2.3	819	2	I48859	tyro 10 receptor k
29	171	2.2	1381	2	T31083	paranodin - rat
30	171	2.2	1385	2	T14158	neurexin IV - mous
31	149.5	1.9	578	2	S66353	L-ascorbate oxidas
32	149	1.9	1883	2	G82875	hypothetical prote
33	148	1.9	622	2	S62580	probable multicopp
34	141.5	1.8	1196	2	S46430	botulinum neurotox
35	140.5	1.8	1196	2	JQ1467	toxin, nontoxic co
36	140.5	1.8	1217	2	T18209	mnxG protein - Bac
37	139	1.8	1193	2	JC4901	nontoxic-nonhemagg
38	137.5	1.8	580	2	F84828	probable laccase (
39	137.5	1.8	903	2	F82080	preprotein translo
40	136.5	1.8	2657	2	T18497	hypothetical prote
41	135	1.8	343	2	T35030	probable copper ox
42	134.5	1.7	791	2	T16031	hypothetical prote
43	134.5	1.7	1132	2	H82887	hypothetical prote
44	133.5	1.7	567	2	T44928	L-ascorbate oxidas
45	133.5	1.7	2925	2	T00133	RNA-directed RNA p

ALIGNMENTS

RESULT 1

EZHU

coagulation factor VIII precursor [validated] - human

N;Alternate names: antihemophilic factor A; coagulation factor VIIIC; procoagulant com
C;Species: Homo sapiens (man)

C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 31-Dec-2004

C;Accession: I54318; A00525; I58059; A23584; A26174; A42348; A43986; S63527; S66445; B
R;Gitschier, J.; Wood, W.I.

Hum. Mol. Genet. 1, 199-200, 1992

A;Title: Sequence of the exon-containing regions of the human factor VIII gene.

A;Reference number: I54318; MUID:93265012; PMID:1303178

A;Accession: I54318

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1921,'S',1923-2351

A;Cross-references: UNIPROT:P00451; UNIPARC:UPI000016A8D3; GB:M88648; NID:g182381; PID
R;Wood, W.I.; Capon, D.J.; Simonsen, C.C.; Eaton, D.L.; Gitschier, J.; Keyt, B.; Seebu
Nature 312, 330-337, 1984

A;Title: Expression of active human factor VIII from recombinant DNA clones.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 10:48:58 ; Search time 335 Seconds
(without alignments)
3970.664 Million cell updates/sec

Title: US-10-511-559-73
Perfect score: 7693
Sequence: 1 ATRRYLGAVELSWDYMQSD.....WVHQIALRMEVLGCEAQDLY 1438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	7236	94.1	2351	1	FA8_HUMAN	P00451 h coagulati
2	7236	94.1	2351	2	Q5HY69_HUMAN	Q5hy69 homo sapien
3	6281	81.6	2343	1	FA8_CANFA	O18806 canis famil
4	6236	81.1	2133	1	FA8_PIG	P12263 sus scrofa

5	6201	80.6	2319	1	FA8_MOUSE	Q06194	mus musculus
6	4967.5	64.6	2258	2	Q7TN96_RAT	Q7tn96	rattus norv
7	3236	42.1	1639	2	Q804W6_FUGRU	Q804w6	fugu rubrip
8	2672.5	34.7	1459	2	Q593B6_PSETE	Q593b6	pseudonaja
9	2652	34.5	1460	2	Q7SZN0_PSETE	Q7szn0	pseudonaja
10	2650.5	34.5	1459	2	Q58L91_9SAUR	Q58l91	oxyuranus s
11	2641	34.3	1458	2	Q49MF1_OXYSC	Q49mf1	oxyuranus s
12	2631	34.2	1460	2	Q58L90_OXYMI	Q58l90	oxyuranus m
13	2542	33.0	1802	2	Q804W5_FUGRU	Q804w5	fugu rubrip
14	2490.5	32.4	2119	2	Q90X47_BRARE	Q90x47	brachydanio
15	2394.5	31.1	2224	1	FA5_HUMAN	P12259	homo sapien
16	2387.5	31.0	2224	2	Q5R347_HUMAN	Q5r347	homo sapien
17	2380	30.9	1304	2	Q4RPE7_TETNG	Q4rpe7	tetraodon n
18	2375	30.9	2229	2	Q5R346_HUMAN	Q5r346	homo sapien
19	2371	30.8	2183	2	O88783_MOUSE	O88783	mus musculus
20	2370	30.8	2211	1	FA5_BOVIN	Q28107	bos taurus
21	2355.5	30.6	2258	1	FA5_PIG	Q9glp1	sus scrofa
22	2326.5	30.2	1377	2	Q804X3_CHICK	Q804x3	gallus gall
23	2093	27.2	1725	2	Q4S9Q1_TETNG	Q4s9q1	tetraodon n
24	1809	23.5	1157	1	HEPH_MOUSE	Q9z0z4	mus musculus
25	1793	23.3	1157	1	HEPH_RAT	Q920h8	rattus norv
26	1751	22.8	1158	1	HEPH_HUMAN	Q9bqs7	homo sapien
27	1751	22.8	1158	2	Q5JU00_HUMAN	Q5juu0	homo sapien
28	1740	22.6	1087	2	Q7ZU12_BRARE	Q7zu12	brachydanio
29	1739	22.6	1087	2	Q6P3G1_BRARE	Q6p3g1	brachydanio
30	1736.5	22.6	1065	1	CERU_HUMAN	P00450	homo sapien
31	1736.5	22.6	1065	2	Q2PP18_HUMAN	Q2pp18	homo sapien
32	1718.5	22.3	1084	2	Q9JL97_RAT	Q9jl97	rattus norv
33	1696	22.0	1048	2	Q4T8Z9_TETNG	Q4t8z9	tetraodon n
34	1693.5	22.0	1059	1	CERU_RAT	P13635	rattus norv
35	1684	21.9	1061	2	Q6P5C8_MOUSE	Q6p5c8	mus musculus
36	1644.5	21.4	1062	1	CERU_MOUSE	Q61147	mus musculus
37	1627	21.1	1048	2	Q9XT27_SHEEP	Q9xt27	ovis aries
38	1601.5	20.8	349	2	Q684Q7_MOUSE	Q684q7	mus musculus
39	1599.5	20.8	2102	2	Q7TPK2_RAT	Q7tpk2	rattus norv
40	1589.5	20.7	1007	2	Q4SFU7_TETNG	Q4sfu7	tetraodon n
41	1543.5	20.1	355	2	Q8BQ43_MOUSE	Q8bq43	mus musculus
42	1489.5	19.4	911	2	Q3VLH3_MOUSE	Q3vlh3	mus musculus
43	1443.5	18.8	745	2	Q804X4_CHICK	Q804x4	gallus gall
44	1408	18.3	709	2	Q32PR1_BRARE	Q32pr1	brachydanio
45	1341	17.4	891	2	Q5JU01_HUMAN	Q5juu1	homo sapien

ALIGNMENTS

RESULT 1

FA8_HUMAN

ID FA8_HUMAN STANDARD; PRT; 2351 AA.

AC P00451;

DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.

DT 21-JUL-1986, sequence version 1.

DT 07-FEB-2006, entry version 96.

DE Coagulation factor VIII precursor (Procoagulant component)

DE (Antihemophilic factor) (AHF) [Contains: Factor VIIIA heavy chain, 200

DE kDa isoform; Factor VIIIA heavy chain, 92 kDa isoform; Factor VIII B

DE chain; Factor VIIIA light chain].

GN Name=F8; Synonyms=F8C;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:15:39 ; Search time 198 Seconds
(without alignments)
34.638 Million cell updates/sec

Title: US-10-511-559-73_COPY_817_831
Perfect score: 75
Sequence: 1 MSSSPHVLNRNAQSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	75	100.0	15	7	ADM75918	Adm75918 Human MHC
2	75	100.0	15	7	ADM75967	Adm75967 Human MHC
3	75	100.0	15	7	ADM75952	Adm75952 Human MHC
4	75	100.0	15	7	ADM75974	Adm75974 Human Fac
5	75	100.0	15	8	ADG06422	Adg06422 Human B-d
6	75	100.0	20	5	ABJ05003	Abj05003 A3 peptid
7	75	100.0	60	5	ABJ04948	Abj04948 A3 domain
8	75	100.0	642	6	ABP60515	Abp60515 Human fac
9	75	100.0	643	6	ABP60514	Abp60514 Human fac
10	75	100.0	684	2	AAR73022	Aar73022 Human Fac
11	75	100.0	684	2	AAR74091	Aar74091 Factor-VI
12	75	100.0	770	3	ADP20767	Adp20767 Factor VI
13	75	100.0	790	5	ADE64594	Ade64594 Recombina
14	75	100.0	1283	3	AAB07205	Aab07205 Human Fac
15	75	100.0	1284	1	AAP50108	Aap50108 Factor-VI
16	75	100.0	1383	2	AAW33227	Aaw33227 Procoagul
17	75	100.0	1383	2	AAW33228	Aaw33228 Procoagul
18	75	100.0	1383	2	AAW33229	Aaw33229 Procoagul
19	75	100.0	1402	8	ADU47620	Adu47620 Human fac
20	75	100.0	1421	8	ADQ37613	Adq37613 Human Fac
21	75	100.0	1421	8	ADQ37598	Adq37598 Human Fac
22	75	100.0	1422	8	ADQ37591	Adq37591 Human Fac
23	75	100.0	1422	8	ADQ37606	Adq37606 Human Fac
24	75	100.0	1423	8	ADU47614	Adu47614 Human fac
25	75	100.0	1424	1	AAP80268	Aap80268 Modified
26	75	100.0	1424	1	AAP91169	Aap91169 Sequence
27	75	100.0	1424	4	AAB48842	Aab48842 Mutant ma
28	75	100.0	1424	5	AAO18622	Aao18622 Human mat
29	75	100.0	1424	9	ADZ65051	Adz65051 Human mat
30	75	100.0	1425	1	AAP80267	Aap80267 Modified
31	75	100.0	1425	8	ADQ37605	Adq37605 Human Fac
32	75	100.0	1425	8	ADQ37590	Adq37590 Human Fac
33	75	100.0	1426	8	ADU47612	Adu47612 Human fac
34	75	100.0	1428	8	ADQ37599	Adq37599 Human Fac
35	75	100.0	1428	8	ADQ37604	Adq37604 Human Fac
36	75	100.0	1428	8	ADQ37589	Adq37589 Human Fac
37	75	100.0	1428	8	ADQ37614	Adq37614 Human Fac
38	75	100.0	1434	8	ADQ37594	Adq37594 Human Fac
39	75	100.0	1434	8	ADQ37609	Adq37609 Human Fac
40	75	100.0	1435	8	ADQ37600	Adq37600 Human Fac
41	75	100.0	1435	8	ADQ37615	Adq37615 Human Fac
42	75	100.0	1437	8	ADQ37593	Adq37593 Human Fac
43	75	100.0	1437	8	ADQ37608	Adq37608 Human Fac
44	75	100.0	1438	3	AAB01262	Aab01262 B-domain
45	75	100.0	1438	7	ADF31316	Adf31316 Variant o
46	75	100.0	1438	7	ADM75988	Adm75988 Modified
47	75	100.0	1438	7	ADM75985	Adm75985 Modified
48	75	100.0	1438	7	ADM75986	Adm75986 Modified
49	75	100.0	1438	7	ADM75983	Adm75983 Wild-type
50	75	100.0	1438	7	ADM75984	Adm75984 Modified
51	75	100.0	1438	7	ADM75987	Adm75987 Modified
52	75	100.0	1440	2	AAR12971	Aar12971 Factor VI
53	75	100.0	1440	8	ADQ37607	Adq37607 Human Fac
54	75	100.0	1440	8	ADQ37592	Adq37592 Human Fac
55	75	100.0	1441	8	ADQ37612	Adq37612 Human Fac
56	75	100.0	1441	8	ADQ37597	Adq37597 Human Fac
57	75	100.0	1442	8	ADQ37616	Adq37616 Human Fac

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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:24:52 ; Search time 51 Seconds
(without alignments)
25.744 Million cell updates/sec

Title: US-10-511-559-73_COPY_817_831
Perfect score: 75
Sequence: 1 MSSSPHVLNRNAQSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Length	ID	Description
------------	-------	-------------	----------	----	-------------

1	75	100.0	1438	2	US-09-209-916-1	Sequence 1, Appli
2	75	100.0	1445	2	US-09-407-605-3	Sequence 3, Appli
3	75	100.0	1447	2	US-09-407-605-4	Sequence 4, Appli
4	75	100.0	1457	2	US-09-001-039B-47	Sequence 47, Appl
5	75	100.0	1471	1	US-08-683-839B-3	Sequence 3, Appli
6	75	100.0	1661	1	US-08-882-083-2	Sequence 2, Appli
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15	75	100.0	2332	2	US-09-037-601-2	Sequence 2, Appli
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25	75	100.0	2351	1	US-08-121-202-2	Sequence 2, Appli
26	75	100.0	2351	1	US-08-366-851A-2	Sequence 2, Appli
27	75	100.0	2351	2	US-10-133-907-4	Sequence 4, Appli
28	75	100.0	2351	2	US-09-001-039B-45	Sequence 45, Appl
29	75	100.0	2351	7	5171844-2	Patent No. 5171844
30	75	100.0	2351	7	5422260-1	Patent No. 5422260
31	69	92.0	2343	2	US-09-324-867-2	Sequence 2, Appli
32	56	74.7	16	1	US-08-480-190-170	Sequence 170, App
33	56	74.7	16	1	US-08-488-379-170	Sequence 170, App
34	56	74.7	16	2	US-08-475-399A-170	Sequence 170, App
35	56	74.7	16	2	US-08-077-255A-170	Sequence 170, App
36	56	74.7	16	5	PCT-US93-07545-170	Sequence 170, App
37	56	74.7	868	1	US-07-864-004B-6	Sequence 6, Appli
38	56	74.7	868	1	US-08-251-937A-6	Sequence 6, Appli
39	56	74.7	868	1	US-08-212-133A-3	Sequence 3, Appli
40	56	74.7	1090	5	PCT-US93-03275-6	Sequence 6, Appli
41	56	74.7	1443	1	US-08-670-707A-39	Sequence 39, Appl
42	56	74.7	1443	2	US-09-037-601-39	Sequence 39, Appl
43	56	74.7	1443	2	US-09-315-179-39	Sequence 39, Appl
44	56	74.7	1443	3	US-10-187-319-39	Sequence 39, Appl
45	56	74.7	1443	3	US-10-131-510A-39	Sequence 39, Appl
46	56	74.7	1467	2	US-09-523-656-38	Sequence 38, Appl
47	56	74.7	2115	2	US-09-324-867-5	Sequence 5, Appli
48	56	74.7	2133	1	US-08-670-707A-37	Sequence 37, Appl
49	56	74.7	2133	2	US-09-037-601-37	Sequence 37, Appl
50	56	74.7	2133	2	US-09-315-179-37	Sequence 37, Appl
51	56	74.7	2133	2	US-09-523-656-30	Sequence 30, Appl
52	56	74.7	2133	3	US-10-187-319-37	Sequence 37, Appl
53	56	74.7	2133	3	US-10-131-510A-37	Sequence 37, Appl
54	43	57.3	2304	2	US-09-324-867-4	Sequence 4, Appli
55	43	57.3	2319	1	US-08-212-133A-8	Sequence 8, Appli
56	43	57.3	2319	1	US-08-474-503-6	Sequence 6, Appli
57	43	57.3	2319	1	US-08-670-707A-6	Sequence 6, Appli
58	43	57.3	2319	2	US-09-037-601-6	Sequence 6, Appli
59	43	57.3	2319	2	US-09-315-179-6	Sequence 6, Appli
60	43	57.3	2319	2	US-09-523-656-28	Sequence 28, Appl

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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:36:35 ; Search time 180 Seconds
(without alignments)
38.601 Million cell updates/sec

Title: US-10-511-559-73_COPY_817_831
Perfect score: 75
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	75	100.0	15	5	US-10-511-559-80	Sequence 80, Appl
2	75	100.0	15	6	US-11-009-460-109	Sequence 109, App
3	75	100.0	20	4	US-10-433-273-59	Sequence 59, Appl
4	75	100.0	60	4	US-10-433-273-4	Sequence 4, Appli
5	75	100.0	1424	5	US-10-472-516-5	Sequence 5, Appli
6	75	100.0	1424	5	US-10-968-286-5	Sequence 5, Appli
7	75	100.0	1438	4	US-10-006-091-1	Sequence 1, Appli
8	75	100.0	1438	4	US-10-047-257-1	Sequence 1, Appli
9	75	100.0	1438	4	US-10-225-900-1	Sequence 1, Appli
10	75	100.0	1438	5	US-10-511-559-73	Sequence 73, Appl
11	75	100.0	1457	5	US-10-813-507-13	Sequence 13, Appl
12	75	100.0	1457	5	US-10-813-507-17	Sequence 17, Appl
13	75	100.0	1459	4	US-10-239-498A-4	Sequence 4, Appli
14	75	100.0	1459	4	US-10-239-498A-13	Sequence 13, Appl
15	75	100.0	1459	4	US-10-239-498A-15	Sequence 15, Appl
16	75	100.0	1471	4	US-10-095-718-2	Sequence 2, Appli
17	75	100.0	1471	4	US-10-681-970-2	Sequence 2, Appli
18	75	100.0	2096	5	US-10-741-600-1032	Sequence 1032, Ap
19	75	100.0	2096	5	US-10-995-561-606	Sequence 606, App
20	75	100.0	2332	3	US-09-957-641-2	Sequence 2, Appli
21	75	100.0	2332	4	US-10-187-319-2	Sequence 2, Appli
22	75	100.0	2332	4	US-10-131-510A-2	Sequence 2, Appli
23	75	100.0	2332	4	US-10-445-235-2	Sequence 2, Appli
24	75	100.0	2332	4	US-10-360-101-229	Sequence 229, App
25	75	100.0	2332	4	US-10-239-498A-2	Sequence 2, Appli
26	75	100.0	2332	4	US-10-466-998A-1	Sequence 1, Appli
27	75	100.0	2332	4	US-10-353-753-1	Sequence 1, Appli
28	75	100.0	2332	4	US-10-721-997A-34	Sequence 34, Appl
29	75	100.0	2332	5	US-10-789-956-2	Sequence 2, Appli
30	75	100.0	2332	5	US-10-491-464-2	Sequence 2, Appli
31	75	100.0	2332	5	US-10-938-414-2	Sequence 2, Appli
32	75	100.0	2332	5	US-10-813-507-6	Sequence 6, Appli
33	75	100.0	2332	5	US-10-973-941-2	Sequence 2, Appli
34	75	100.0	2351	4	US-10-132-829-4	Sequence 4, Appli
35	75	100.0	2351	4	US-10-172-712-27	Sequence 27, Appl
36	75	100.0	2351	4	US-10-133-907-4	Sequence 4, Appli
37	75	100.0	2351	4	US-10-411-037-30	Sequence 30, Appl
38	75	100.0	2351	4	US-10-411-026-30	Sequence 30, Appl
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41	75	100.0	2351	4	US-10-410-930-30	Sequence 30, Appl
42	75	100.0	2351	4	US-10-410-997-30	Sequence 30, Appl
43	75	100.0	2351	4	US-10-411-012-30	Sequence 30, Appl
44	75	100.0	2351	4	US-10-287-994-30	Sequence 30, Appl
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48	75	100.0	2351	5	US-10-741-600-1034	Sequence 1034, Ap
49	75	100.0	2351	5	US-10-410-980-30	Sequence 30, Appl
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51	75	100.0	2351	5	US-10-968-286-2	Sequence 2, Appli
52	75	100.0	2351	5	US-10-492-261-30	Sequence 30, Appl
53	75	100.0	2351	5	US-10-995-561-608	Sequence 608, App
54	75	100.0	2351	6	US-11-183-205-30	Sequence 30, Appl
55	75	100.0	2351	6	US-11-244-087-3	Sequence 3, Appli
56	75	100.0	2351	6	US-11-267-631-49	Sequence 49, Appl
57	69	92.0	1431	4	US-10-095-718-4	Sequence 4, Appli
58	69	92.0	1431	4	US-10-681-970-4	Sequence 4, Appli
59	65	86.7	13	5	US-10-511-559-831	Sequence 831, App
60	64	85.3	13	5	US-10-511-559-832	Sequence 832, App
61	58	77.3	13	5	US-10-511-559-833	Sequence 833, App

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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:36:39 ; Search time 15 Seconds
(without alignments)
11.137 Million cell updates/sec

Title: US-10-511-559-73_COPY_817_831
Perfect score: 75
Sequence: 1 MSSSPHVLNRNRAQSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*
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3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
Query

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1	75	100.0	1457	7	US-11-280-757-37	Sequence 37, Appl
2	75	100.0	2351	7	US-11-183-218-30	Sequence 30, Appl
3	75	100.0	2351	7	US-11-280-757-35	Sequence 35, Appl
4	38	50.7	245	6	US-10-953-349-37574	Sequence 37574, A
5	38	50.7	462	6	US-10-953-349-32051	Sequence 32051, A
6	37	49.3	862	6	US-10-199-229-14	Sequence 14, Appl
7	37	49.3	875	6	US-10-199-229-10	Sequence 10, Appl
8	37	49.3	1167	7	US-11-121-154-1	Sequence 1, Appli
9	36	48.0	165	6	US-10-953-349-38626	Sequence 38626, A
10	35	46.7	234	6	US-10-953-349-33666	Sequence 33666, A
11	35	46.7	240	6	US-10-953-349-16702	Sequence 16702, A
12	35	46.7	273	6	US-10-953-349-33665	Sequence 33665, A
13	35	46.7	356	6	US-10-953-349-33664	Sequence 33664, A
14	35	46.7	374	6	US-10-953-349-2190	Sequence 2190, Ap
15	35	46.7	380	6	US-10-953-349-2189	Sequence 2189, Ap
16	35	46.7	460	6	US-10-953-349-32416	Sequence 32416, A
17	35	46.7	517	6	US-10-953-349-32415	Sequence 32415, A
18	35	46.7	558	6	US-10-953-349-32414	Sequence 32414, A
19	35	46.7	1807	6	US-10-504-120-22	Sequence 22, Appl
20	34	45.3	190	6	US-10-953-349-26757	Sequence 26757, A
21	34	45.3	230	6	US-10-953-349-26790	Sequence 26790, A
22	34	45.3	251	6	US-10-953-349-26789	Sequence 26789, A
23	34	45.3	365	6	US-10-953-349-331	Sequence 331, App
24	34	45.3	376	6	US-10-953-349-330	Sequence 330, App
25	34	45.3	385	6	US-10-953-349-423	Sequence 423, App
26	34	45.3	386	6	US-10-953-349-13553	Sequence 13553, A
27	34	45.3	386	6	US-10-953-349-17965	Sequence 17965, A
28	34	45.3	392	6	US-10-953-349-422	Sequence 422, App
29	34	45.3	393	6	US-10-953-349-329	Sequence 329, App
30	34	45.3	409	6	US-10-953-349-421	Sequence 421, App
31	34	45.3	417	6	US-10-953-349-13552	Sequence 13552, A
32	34	45.3	417	6	US-10-953-349-17964	Sequence 17964, A
33	34	45.3	777	7	US-11-293-697-3189	Sequence 3189, Ap
34	34	45.3	1237	7	US-11-325-764-32	Sequence 32, Appl
35	33.5	44.7	205	6	US-10-953-349-15363	Sequence 15363, A
36	33.5	44.7	206	6	US-10-953-349-28535	Sequence 28535, A
37	33	44.0	188	6	US-10-953-349-36581	Sequence 36581, A
38	33	44.0	194	6	US-10-953-349-2806	Sequence 2806, Ap
39	33	44.0	205	7	US-11-293-697-4682	Sequence 4682, Ap
40	33	44.0	259	6	US-10-953-349-12424	Sequence 12424, A
41	33	44.0	260	6	US-10-953-349-12423	Sequence 12423, A
42	33	44.0	270	6	US-10-953-349-21274	Sequence 21274, A
43	33	44.0	272	6	US-10-953-349-19371	Sequence 19371, A
44	33	44.0	301	6	US-10-953-349-6479	Sequence 6479, Ap
45	33	44.0	301	7	US-11-293-697-2835	Sequence 2835, Ap
46	33	44.0	307	6	US-10-953-349-24822	Sequence 24822, A
47	33	44.0	309	6	US-10-953-349-6478	Sequence 6478, Ap
48	33	44.0	312	6	US-10-953-349-21273	Sequence 21273, A
49	33	44.0	316	6	US-10-953-349-19370	Sequence 19370, A
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51	33	44.0	333	6	US-10-953-349-15724	Sequence 15724, A
52	33	44.0	333	6	US-10-953-349-30308	Sequence 30308, A
53	33	44.0	334	6	US-10-953-349-15723	Sequence 15723, A
54	33	44.0	339	6	US-10-953-349-12422	Sequence 12422, A
55	33	44.0	351	7	US-11-293-697-4554	Sequence 4554, Ap
56	33	44.0	366	6	US-10-953-349-24821	Sequence 24821, A
57	33	44.0	368	6	US-10-953-349-21272	Sequence 21272, A
58	33	44.0	425	6	US-10-953-349-20579	Sequence 20579, A
59	33	44.0	461	6	US-10-953-349-20578	Sequence 20578, A

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C;Species: Synechocystis sp. A;Variety: PCC 6803 C;Date: 25-Apr-1997 #sequence_revision 25-A
cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and
the EMBL Data Library, June 1996 C;Genetics: A;Gene: dnaJ A;Start codon: GTG F;24-91/Domain:
1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004 C;Accession: S46093 R;Dubois,
SGD:APG12; MIPS:YBR217w A;Cross-references: SGD:S0000421 A;Map position: 2R C;Superfamil
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SSPHVLQN 176 RESULT 20 E84504 hypothetical protein At2g12910 [imported] - Arabidopsis thalia
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PIDN:AAD20650.1; GSPDB:GN00139 C;Genetics: A;Gene: At2g12910 A;Map position: 2 C;Superfa
C;Accession: A54277; S60344 R;Eckner, R.; Ewen, M.E.; Newsome, D.; Gerdes, M.; DeCaprio, J.A
GB:U01877; NID:g495300; PIDN:AAA18639.1; PID:g495301 A;Note: in the authors' translation 94
552-660 A;Cross-references: UNIPARC:UPI00001782EB C;Genetics: A;Gene: GDB:EP300 A;Cross-
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G89787 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-698 A;Cross-references: UNIPF
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Goldsmith, A.D.; Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A;Autl
Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L.J.; Tambunga, G.; Toriumi, M.J.; To
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K.; Hirakawa, H.; Kuhara, S.; Goto, S.; Yabuzaki, J.; Kanehisa, M.; Yamashita, A.; Oshima, K.; Fur
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Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Nature 391, 485-488, 199
sequence from chromosome 4 of Arabidopsis thaliana. A;Reference number: A71400; MUID:98121
45.5%; Pred. No. 1.8e+02; Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0; Qy 1 MS
K.F.X. submitted to the Protein Sequence Database, April 2000 A;Reference number: Z24460 A;Ac
Indels 0; Gaps 0; Qy 4 SPHVLNRNAQ 13 :||:| |||: Db 920 APHLLNRRAR 929 RESULT 32 T33123 hy
type: DNA A;Residues: 1-2275 A;Cross-references: UNIPARC:UPI000017B6FD; EMBL:AF067608; F
70.0%; Pred. No. 4.1e+02; Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Qy 5 PHV
Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A;Title: The complete genome sequer
acetyltransferase Query Match 48.7%; Score 36.5; DB 2; Length 394; Best Local Similarity 55.6%.
B.; Glasner, J.D.; Rose, D.J.; Mayhew, G.F.; Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.; Posfai, G.; I

A;Residues: 1-394 A;Cross-references: UNIPROT:Q8X6I7; UNIPARC:UPI00000D0B7A; GB:AE0051 E91091 probable acyltransferase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 05) Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison of acetyltransferase Query Match 48.7%; Score 36.5; DB 2; Length 394; Best Local Similarity 55.6%.

A;Reference number: S44153 A;Accession: S44153 A;Status: preliminary A;Molecule type: DNA A; Sinorhizobium meliloti (strain 1021) magaplasamid pSymA C;Species: Sinorhizobium meliloti C;Date: 9883-9888, 2001 A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium Hubler, F.; Barnett, M.J.; Becker, A.; Boistard, P.; Bothe, G.; Boutry, M.; Bowser, L.; Buhrmester, Surzycki, R.; Thebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh

RESULT 38 F83097 probable two-component response regulator PA4381 [imported] - Pseudomona Smith, K.A.; Spencer, D.H.; Wong, G.K.S.; Wu, Z.; Paulsen, I.T.; Reizer, J.; Saier, M.H.; Hancock, GSPDB:GN00131; PASP:PA4381 A;Experimental source: strain PAO1 C;Genetics: A;Gene: PA4381 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004 C;Accession: G83948 R;Takami, H.

A;Residues: 1-242 A;Cross-references: UNIPROT:Q9KA99; UNIPARC:UPI00000C3ECC; GB:AP0015 fructose-bisphosphate aldolase (EC 4.1.2.13) F19H22.70 - Arabidopsis thaliana C;Species: Arabido EMBL:AL035679; GSPDB:GN00062; ATSP:F19H22.70 A;Experimental source: cultivar Columbia; B. AC3603 3-methyl-2-oxobutanoate dehydrogenase (lipoamide) (EC 1.2.4.4) [imported] - Brucella m R.; Kyripides, N.; Overbeek, R. Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002 A;Title: The genom dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-binding domain homology C;Keyw R;McMurray, A. submitted to the EMBL Data Library, May 1996 A;Reference number: Z19128 A;Ac Best Local Similarity 75.0%; Pred. No. 1e+02; Matches 6; Conservative 1; Mismatches 1; Indels 0

Read, T.D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Drag references: UNIPROT:Q9KP44; UNIPARC:UPI00000C3316; GB:AE004322; GB:AE003852; NID:g96

RESULT 44 A71302 conserved hypothetical protein TP0624 - syphilis spirochete C;Species: Trepon P.; Bowman, C.; Cotton, M.D.; Fujii, C.; Garland, S.; Hatch, B.; Horst, K.; Roberts, K.; Watthey, L. A;Cross-references: UNIPROT:O83632; UNIPARC:UPI00000C0A97; GB:AE001237; GB:AE000520; herpesvirus 6 A;Variety: strain Z29 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_ A;Cross-references: UNIPROT:P52454; UNIPARC:UPI0000137B3C; EMBL:AF157706; PIDN:AAB063

herpesvirus 6 A;Variety: strain HST C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_ GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-662 A;Cross-references: UNIPROT:O57138; L DNA excision/repair protein, SNF2 and RAD26 DRP1 [imported] - Leishmania major (strain Friedlin of protein-coding genes. A;Reference number: A81455; MUID:99178987; PMID:10077609 A;Acces Mismatches 3; Indels 0; Gaps 0; Qy 2 SSSPHVLRNRAQSG 15 |::|||: : ::| Db 39 STSPHVVSQRPRAC GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-974 A;Cross-references: UNIPROT:Q23463; L Conservative 3; Mismatches 2; Indels 0; Gaps 0; Qy 5 PHVLRNRAQSG 15 ||::|| | :| Db 129 PHIMR GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1173 A;Cross-references: UNIPROT:P92199; 3.1e+02; Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0; Qy 4 SPHVLRNRAQ 13 || || A;Description: Genomic sequence of BAC T4I9 from Arabidopsis thaliana, chromosome IV, near 16 1456; Best Local Similarity 60.0%; Pred. No. 3.9e+02; Matches 6; Conservative 2; Mismatches 2;

GenCore version 5.1.8

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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:19:54 ; Search time 38 Seconds
(without alignments)
37.980 Million cell updates/sec

Title: US-10-511-559-73_COPY_817_831
Perfect score: 75
Sequence: 1 MSSSPHVLRNRAQSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	75	100.0	2351	1	EZHU	coagulation factor
2	56	74.7	869	2	A25945	coagulation factor
3	56	74.7	2133	2	T42763	coagulation factor
4	50	66.7	440	2	G82426	probable phosphogl
5	43	57.3	2319	2	A47004	coagulation factor
6	42	56.0	355	1	S22181	gamma-l-microglobu
7	40	53.3	133	2	JC7103	endo-1,4-beta-xyla
8	40	53.3	390	2	F83220	hypothetical prote
9	40	53.3	584	2	H95336	probable adenylate
10	40	53.3	616	2	B33586	C4-dicarboxylate t
11	40	53.3	621	2	D96032	C4-dicarboxylate t
12	39	52.0	88	2	C84469	hypothetical prote
13	39	52.0	312	2	B86494	integrase/recombin
14	39	52.0	312	2	F72129	integrase/recombin
15	39	52.0	443	2	I38603	heme A farnesyltra
16	38	50.7	101	2	D70710	hypothetical prote
17	38	50.7	174	2	S74666	DnaJ protein - Syn
18	38	50.7	186	2	S46093	probable membrane
19	38	50.7	405	2	JC5175	seed storage prote
20	38	50.7	567	2	E84504	hypothetical prote
21	38	50.7	2414	2	A54277	transcription adap
22	38	50.7	2441	2	S39161	CREB-binding prote
23	37.5	50.0	698	2	G89787	hypothetical prote
24	37	49.3	133	2	A86283	hypothetical prote
25	37	49.3	138	2	AE1089	Antigen C homolog
26	37	49.3	361	2	AG0335	chorismate synthas
27	37	49.3	383	2	G89902	competence-damage
28	37	49.3	392	2	T51772	acetyl-CoA C-acety
29	37	49.3	650	2	T15972	hypothetical prote
30	37	49.3	1052	2	E71422	hypothetical prote
31	37	49.3	1256	2	T47325	hypothetical prote
32	37	49.3	2275	2	T33123	hypothetical prote
33	36.5	48.7	394	2	E65067	hypothetical prote
34	36.5	48.7	394	2	H85936	probable acyltrans
35	36.5	48.7	394	2	E91091	probable acyltrans
36	36	48.0	62	2	S44153	hypothetical prote

SCORE Search Results Details for Application 10511559 and Search Result us-10-511-559-73_copy_817_831.rup.

[Score Home](#) [Retrieve Application](#) [SCORE System](#) [SCORE](#) [Comments /](#)
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This page gives you Search Results detail for the Application 10511559 and Search Result us-10-511-559-73_copy_817_831.rup.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:15:52 ; Search time 296 Seconds
(without alignments)
46.876 Million cell updates/sec

Title: US-10-511-559-73_COPY_817_831
Perfect score: 75
Sequence: 1 MSSSPHVLNRNRAQSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	75	100.0	2351	1	FA8_HUMAN P00451 h coagulati
2	75	100.0	2351	2	Q5HY69_HUMAN Q5hy69 homo sapien
3	69	92.0	2343	1	FA8_CANFA O18806 canis famil
4	56	74.7	2133	1	FA8_PIG P12263 sus scrofa

5	50	66.7	313	2	Q5DBY4_SCHJA	Q5dby4	schistosoma
6	50	66.7	440	2	Q9KLN7_VIBCH	Q9kln7	vibrio chol
7	49	65.3	288	2	Q5LLG7_SILPO	Q5llg7	silicibacte
8	46	61.3	332	2	Q55R49_CRYNE	Q55r49	cryptococcu
9	46	61.3	355	2	Q5KF20_CRYNE	Q5kf20	cryptococcu
10	44	58.7	473	2	Q3CGK8_THEET	Q3cgk8	thermoanaer
11	43	57.3	282	2	Q3JWP8_BURP1	Q3jwp8	burkholderi
12	43	57.3	282	2	Q62MY6_BURMA	Q62my6	burkholderi
13	43	57.3	282	2	Q63Y07_BURPS	Q63y07	burkholderi
14	43	57.3	290	2	Q7VZE1_BORPE	Q7vze1	bordetella
15	43	57.3	290	2	Q7WGW7_BORBR	Q7wgw7	bordetella
16	43	57.3	597	2	Q420I1_DESHA	Q420i1	desulfitoba
17	43	57.3	2319	1	FA8_MOUSE	Q06194	mus musculu
18	42	56.0	206	2	Q5Z752_ORYSA	Q5z752	oryza sativ
19	42	56.0	355	1	AMBP_PLEPL	P36992	pleuronecte
20	42	56.0	382	2	Q36R03_MARHY	Q36r03	marinobacte
21	42	56.0	399	2	Q485V8_COLP3	Q485v8	colwellia p
22	42	56.0	827	2	Q4R3D7_MACFA	Q4r3d7	macaca fasc
23	42	56.0	1742	2	Q32WC7_9VIRU	Q32wc7	dulcamara m
24	41	54.7	139	2	Q2J3U5_RHOPA	Q2j3u5	rhodopseudo
25	41	54.7	349	2	Q8D3B4_WIGBR	Q8d3b4	wiggleswort
26	41	54.7	366	2	Q31FE3_THICR	Q31fe3	thiomicrosp
27	41	54.7	1155	2	Q54NV0_DICDI	Q54nv0	dictyosteli
28	41	54.7	1846	2	Q4WU73_ASPFU	Q4wu73	aspergillus
29	40	53.3	69	2	Q6K254_ORYSA	Q6k254	oryza sativ
30	40	53.3	133	2	Q9Z490_9BACI	Q9z490	bacillus sp
31	40	53.3	160	1	RUVX_GLUOX	Q5fnd1	gluconobact
32	40	53.3	166	2	Q6IGV6_DROME	Q6igv6	drosophila
33	40	53.3	254	2	Q2R8P0_ORYSA	Q2r8p0	oryza sativ
34	40	53.3	356	2	O86865_STRGA	O86865	streptomyce
35	40	53.3	390	2	Q9HYK3_PSEAE	Q9hyk3	pseudomonas
36	40	53.3	405	2	Q46TI9_RALEJ	Q46ti9	ralstonia e
37	40	53.3	423	2	Q3RWW9_RALME	Q3rww9	ralstonia m
38	40	53.3	439	2	Q820M8_NITEU	Q820m8	nitrosomona
39	40	53.3	462	2	Q3FC44_9BURK	Q3fc44	burkholderi
40	40	53.3	462	2	Q44U36_9BURK	Q44u36	burkholderi
41	40	53.3	462	2	Q4LJ36_9BURK	Q4lj36	burkholderi
42	40	53.3	462	2	Q394B7_BURS3	Q394b7	burkholderi
43	40	53.3	472	2	Q5ZR27_CAEEL	Q5zr27	caenorhabdi
44	40	53.3	584	2	Q92Z92_RHIME	Q92z92	rhizobium m
45	40	53.3	621	1	DCTB_RHIME	P13633	rhizobium m
46	40	53.3	642	2	Q4X104_ASPFU	Q4x104	aspergillus
47	40	53.3	711	2	Q6D6D1_ERWCT	Q6d6d1	erwinia car
48	40	53.3	846	2	Q38AP3_9TRYP	Q38ap3	trypanosoma
49	40	53.3	863	2	Q73D59_BACC1	Q73d59	bacillus ce
50	40	53.3	1241	2	Q57WH0_9TRYP	Q57wh0	trypanosoma
51	40	53.3	1823	2	Q90Z25_9TELE	Q90z25	sternopygus
52	40	53.3	2473	2	Q4SSB2_TETNG	Q4ssb2	tetraodon n
53	39.5	52.7	915	2	Q4P1S8_USTMA	Q4pls8	ustilago ma
54	39	52.0	88	2	Q9SL17_ARATH	Q9sl17	arabidopsis
55	39	52.0	136	2	Q3SET3_THIDA	Q3set3	thiobacillu
56	39	52.0	141	2	Q6Z5C7_ORYSA	Q6z5c7	oryza sativ
57	39	52.0	208	2	Q6FT33_CANGA	Q6ft33	candida gla
58	39	52.0	275	2	Q3FAV9_9BURK	Q3fav9	burkholderi
59	39	52.0	282	2	Q2T1N7_BURTH	Q2t1n7	burkholderi
60	39	52.0	288	2	Q3IXE7_RHOS4	Q3ixe7	rhodobacter
61	39	52.0	297	2	Q72TM1_LEPIC	Q72tm1	leptospira
62	39	52.0	297	2	Q8F1M8_LEPIN	Q8flm8	leptospira
63	39	52.0	312	1	XERC_CHLPN	Q9z9f7	chlamydia p
64	39	52.0	349	2	Q2X6P3_9GAMM	Q2x6p3	shewanella
65	39	52.0	349	2	Q2ZAQ5_9GAMM	Q2zaq5	shewanella